SPBC16G5.09: pombe : GeneDB Page 1 of 3

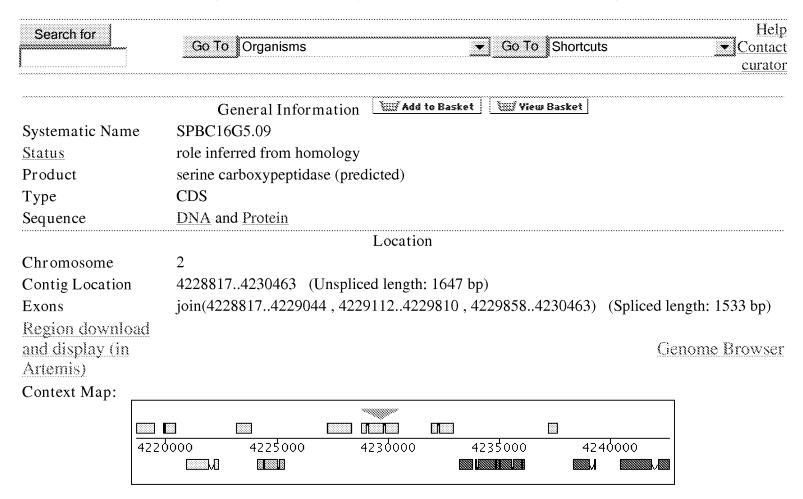


CDS: SPBC16G5.09



WARNING: 30th July 2008

We continue to have problems downloading Boolean search results. We are working to resolve them.



SPBC16G5.03 mrpl23 SPBC16G5.05c SPBC16G5.06 SPBC16G5.07c trp4 >SPBC16G5.09< SPBC16G5.10 bag101 top3 SPBC16G5.13 rps3 fkh2

Term peptidase family S10 predicted N-terminal signal sequence similar to S. cerevisiae YGL203C conserved family Curation Other genes annotated to this term (1 Other) (254 Others) (0 Others) (54 Others)

Predicted Peptide Properties					
Mass	57.6 kDa	Amino acids	510		
Isoelectric point	pH 4.5	Charge	-24.5		
Signal Peptide	Signal peptide predicted for SPBC16G5.09 by SignalP 2.0 HMM (Signal peptide probability 0.961, signal anchor probability 0.003) with cleavage site probability 0.864 between residues 21 and 22				

Transmembrane

http://www.genedb.org/genedb/Dispatcher?formType=navBar&organism=pombe&desc=yes&wildcard=ye... 8/3/2008

Domains 1 probable transmembrane helix predicted for SPBC16G5.09 by TMHMM2.0 at aa 469-491 GPI Anchor Not found				
***************************************	Gene Ontology Annotation			
Term (browse Amigo)	Qualifier Evidence	Other genes annotated to this term		
Biological Process				
proteolysis	IEA (GOA:interprolGO_REF:0000002) with InterPro:IPR001563	228 others		
Cellular Component integral to membrane	IEA (GOA:spkwlGO_REF:0000004) with SP_KW:KW-0812	793 others		
trans-Golgi network vacuole	ISS (PMID:17072883) with SGD:S000003171 IDA (PMID:16823372)	2 others 145 others		
Molecular Function carboxypeptidase D activity	ISS (PMID:17072883) with SGD:S000003171	none		
	Catalytic Activity			
EC 3.4.16.6 : <u>IUBMB</u>				
	Published Expression Profiles			
Gene Expression View	ver Cell Cycle Meiosis Environmental Stress Pheromone Response/Mating			
TranscriptomeViewer	SPBC16G5.09 High-resolution view of transcripts in neighbourhood			
	Literature			
Search for in PubMed				
	Domain Information			
	ructure for this gene product			
View SCOP superfam				
DB Accs	Description			
Pfam <u>PF00450</u>	** *			
MEROPS <u>\$10.007</u> MEROPS				
InterPro IPR001563 Peptidase S10, serine carboxypeptidase				
PRINTS PRO0724 Carboxypeptidase C serine protease (S10) family signature				
ProDom PD001189 ProDom				
Database Cross-References				
DB Accs	Description			
UniProtKB <u>O60123</u>	Carboxypeptidase kex1 precursor (EC 3.4.16.6) (Carboxypeptidase D).			
EMBL CU329671 Schizosaccharomyces pombe chromosome II				
	G5_09 Biotwiki			
Elitiez Gelle	G5.09 NCBI Entrez Gene			
FYSSION SPBC16G5.09 FYSSION				
GermOnline SPBC16G5.09 GermOnline				
NBRP SPBC16G5.09 Fission yeast strain database, National BioResource Project (Japan)				
PIR T39601 PIR				
YOGY <u>SPBC16</u>	G5.09 Retrieval of eukaryotic orthologs			

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UniProtKB Annotation For This Protein

Catalytic Activity Preferential release of a C-terminal arginine or lysine residue.

Function Protease with a carboxypeptidase B-like function involved in killer toxin and alpha-factor

precursor processing (By similarity).

Similarity Belongs to the peptidase S10 family.

Subcellular Location Vacuole membrane; Single-pass type I membrane protein.

Carboxypeptidase (5 others), Complete proteome (4982 others), Glycoprotein

Keywords (169 others), Hydrolase (451 others), Membrane (801 others), Protease (90 others),

Signal (136 others), Transmembrane (651 others), Vacuole (42 others)

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Curator feedback

Technical feedback